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GENETIC DIVERGENCE STUDY IN BOTTLE GOURD [*LAGENARIA SICERARIA* (MOL.) STANDL.]

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ABSTRACT

An experiment was carried out to analyze the genetic diversity, for the yield and its contributing traits in forty-bottle gourd genotypes, at the Main Vegetable Research Station, Anand Agricultural University, Anand, during Kharif, 2015. Forty genotypes of bottle gourds were grouped into seven clusters, through Mahalanobis D2 statistics. The clustering pattern indicated the absence of, relationship between geographical diversity and genetic diversity. The maximum genetic divergence was observed between, cluster II and IV, followed by cluster III and VII. The attributes of fruit weight, followed by total sugar content, length of pedicel, antioxidant activity, fruit length, fruit girth, number of fruits per plant and first female flowering node number contributed much to the total genetic divergence. Based on inter-cluster distances, crossing of the genotypes from cluster II with cluster IV, can lead to broad spectrum of variability in segregating generations, to employ selection for yield improvement.

KEYWORDS: Bottle Gourd, Cluster & Genetic Divergence

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Original Article

INTRODUCTION

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is one of the most valuable members of the family Cucurbitaceae, having a somatic chromosome number 2n=22. It is locally known as *lauki* or *ghiya* and it's an important home garden vegetable. It is a fast growing crop, native to India. India is endowed with the wealth of bottle gourd germplasm, comprising of both wild and cultivated species. It is grown in both rainy and summer seasons, and its fruits are available in the market, throughout the year. Bottle gourd is the largest produced cucurbitaceous vegetables in the world, preferred in both urban and rural population. Bottle gourd is a rich source of minerals and vitamins.

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential, for any successful plant breeding programme. Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and presence of enormous genetic variability. Genetic diversity analysis, among elite germplasm is the prerequisite for selecting, promising genetic diverse lines for desirable traits and to expose genetic distinctness among the genotypes (Ali *et al*., 2008). Assessment of genetic diversity in germplasm collections helps in the categorization

of accessions and useful in assigning genotypes, to specific heterotic groups, to create segregating progenies with maximum genetic variability, for further breeding purposes. Hence, an attempt was made to classify the genotypes, based on D^2 statistics for generating more heterotic cross combinations and ultimately, superior useful hybrids.

MATERIALS AND METHODS

The experimental material consisted of forty genotypes, which were laid out in Randomized Complete Block Design (RCBD), with two replications at the Main Vegetable Research Station, Anand Agricultural University, Anand during the *kharif* of 2015. Each genotype was represented by a single row plot of 5 m long, with 5 plants sown at a distance of 2 m, between rows and 1 m between plants. Observations were recorded from three randomly selected plants, for the characters *viz.,* days of opening of first male flower, days of opening of a first female flower, first male flowering node number, first female flowering node number, days to first picking, length of pedicel, fruit length, fruit girth, fruit weight, number of fruits per plant, fruit yield per plant, total soluble solids, total sugar content, ascorbic acid, antioxidant activity and total chlorophyll content. The data obtained on the above 16 characters was used for cluster analysis and investigated to select the parents for hybridization, using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters, by Tocher's method (Rao, 1952). The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed, by taking the maximum D^2 values between any two populations, in the first row of the table, where D^2 values were arranged in increasing order of magnitude.

RESULT AND DISCUSSIONS

The analysis of variance revealed significant differences, among bottle gourd genotypes for all characters, suggesting considerable genetic variability in the population. Using the estimated D^2 values as the squares of generalized distance, all genotypes were grouped into 7 clusters (**Figure 1**). The cluster I was the largest having 22 genotypes followed by cluster II with 11 genotypes. The cluster III and IV contained 2 genotypes. The clusters, each V, VI and VII contained one genotype each (**Table 1**). The pattern of clustering indicated that there was no association between geographic distribution of genotypes and genetic divergence as the same group consisted of genotypes from diverse locations and the genotypes of same source fell into different groups also. This could be because of there were other forces than geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift, environmental variation, etc. Present result is supported by the findings of Singh *et al.* (2007). Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic diversity.

Table 1: Distribution of 40 Genotypes of Bottle Gourd to Different Clusters on the Basis of D^2-Statistics

Sr. No.	Cluster	Number of genotypes	Name of the genotypes	Source
1	I	22	BGM 1, BGM 5, BGM 22, BGM 24, BGM37, BGM53, BGM85, BGM91, BGM 93, BGM95, BGM 100, BGM 101, BGM 115, BGM 118, BGM 125, BGM 131, BGM 136, ABG 1	AAU, Anand
			DBG 5, DBG 6	Durgapur
			Punjab Long	PAU (Ludhiana)
			Pusa Naveen	IARI, New Delhi

2	II	11	BGM 12, BGM 48, BGM 52, BGM 58, BGM 81, BGM 116, BGM 133, BGM 137	AAU, Anand
			Thar Samriddhi	Bikaner
			NDBG 132, NDBG 517	NDUA&T(Faizabad)
3	III	2	Punjab Komal	PAU (Ludhiana)
			Samrat	MPKV (Rahuri)
4	IV	2	BGM 6, BGM 51	AAU, Anand
5	V	1	BGM 56	AAU, Anand
6	VI	1	BGM 120	AAU, Anand
7	VII	1	BGM 80	AAU, Anand

The average inters and intra cluster distances among the five clusters are presented in **Table 2**. The perusal of intra-cluster and inter-cluster distance revealed that inter-cluster values were greater than intra-cluster distance values. The maximum inter-cluster distance (D=54.29) was found between cluster II and IV, followed by cluster III and VII (D=53.96). The minimum inter-cluster distance was observed between cluster I and II (D=34.23). The intra-cluster distance (D) ranged from 24.76 (cluster IV) to 35.63 (cluster III). The clusters V, VI and VII contained single genotype therefore; their intra-cluster distance was zero. Selection of parents based on large inter-cluster and intra-cluster distances for hybridization work gives a range of useful combination. These results are in general agreement with the findings of Islam (2004), Singh *et al.* (2007) and Bhardwaj *et al.* (2013).

Table 2: Average Intra-Cluster and Inter-Cluster Value for 40 Genotypes of Bottle Gourd

Clusters	I	II	III	IV	V	VI	VII
I	26.86	34.23	39.84	37.31	32.59	36.61	41.312
II		27.49	42.97	54.29	38.64	34.56	42.78
III			35.63	48.87	39.41	48.71	53.96
IV				24.76	36.77	47.15	51.14
V					0	42.42	53.88
VI						0	44.46
VII							0

The mean performance for different clusters of genotypes for yield and its components are presented in **Table 3**. The mean values for other important yield attributing traits *viz.,* fruit girth, and fruit weight, number of fruits per plant and antioxidant activity were depicted appreciably higher for cluster V (40.50 cm), cluster V (1.110 kg), cluster VII (8.45) and cluster VI (0.09%), respectively. While the total sugar content was significantly higher for cluster IV (2.78%) and cluster V (2.20%) than other cluster and character mean value (1.40%). There were different characters which showed superiority with respective clusters so, for further breeding programme breeder should select genotypes from particular clusters according to need of crop improvement programme.

Estimates of inter-cluster and intra-cluster variances, along with the ratio (R^2) of inter-cluster variance to the total variance and the inter-cluster coefficient of variation (CV_b) for 16 characters were worked out. The maximum value of R^2 was observed for fruit weight (0.94), followed by total sugar content (0.87) and length of pedicel (0.74). These traits have maximum contribution towards genetic divergence. Hence, selection of divergent parents based on these characters will be useful for selection in heterosis breeding in bottle gourd. The minimum value for R^2 was observed for first male flowering node number (0.05) depicted minimum contribution of trait towards genetic divergence. From inter-cluster coefficient of variation (CV_b %), it was revealed that the total sugar content (77.85 %) demonstrated an important role in the genetic discrimination of genotypes included under study, while the negligible CV_b value (2.85 %) recorded by day to opening of

first male flower. Mathew *et al.* (2001) reported in high contribution of number of fruits per plant, number of seeds per fruit, length of fruit, average fruit weight, vine length and fruit set percentage towards genetic divergence in bottle gourd.

Table 3: Cluster Means of Different Characters in Bottle Gourd

Cluster	Days to Opening of First Male Flower	Days to Opening of First Female Flower	First Male Flowering Node Number	First Female Flowering Node Number	Days to First Picking	Length of Pedicel (cm)	Fruit Length (cm)	Fruit Girth (cm)	Fruit Weight (kg)	Number of Fruits per Plant	Fruit Yield Per Plant (kg)	Total Soluble Solids (°Brix)	Total Sugar Content (%)	Ascorbic Acid (mg / 100g)	Antioxidant Activity (%)	Total Chlorophyll Content (mg /100 g Fresh Weight)
I	49.58	56.13	6.84	11.99	64.25	12.13	32.55	22.32	0.812	5.68	4.46	3.42	1.67	6.9	0.05	1.44
II	48.99	55.39	7.01	12.89	62.72	11.72	30.65	24.91	0.838	5.29	4.41	3.28	0.70	6.81	0.05	1.37
III	47.83	56.00	6.16	11.41	64.00	17.97	26.72	27.84	0.750	6.67	4.74	2.87	1.23	7.04	0.04	1.27
IV	46.33	55.66	6.83	12.91	64.00	12.67	20.58	25.02	0.685	5.22	3.51	3.60	2.78	6.87	0.07	1.39
V	50.33	55.00	8.83	14.83	64.00	12.1	19.75	40.50	1.110	5.40	5.74	3.70	2.20	7.99	0.06	1.25
VI	47.66	58.67	6.16	10.50	66.50	11.35	43.06	17.18	0.710	5.65	3.94	3.25	0.80	7.99	0.09	1.38
VII	51.50	57.33	7.67	15.33	64.00	9.70	14.10	17.90	0.370	8.45	3.08	4.25	0.51	6.99	0.05	1.16
Mean	49.19	55.96	6.90	12.37	63.85	12.26	30.61	23.66	0.804	5.66	4.40	3.38	1.4	6.94	0.05	1.39
SE. m.	1.12	1.25	0.71	0.83	1.66	0.84	4.52	3.42	0.079	0.55	0.45	0.27	0.22	0.35	0.004	0.10
CD @5 %	3.16	NS	NS	2.35	NS	2.38	12.77	9.65	0.225	1.55	1.28	NS	0.64	NS	0.01	NS
CV %	4.19	4.11	19.04	12.42	4.78	12.65	27.19	26.61	18.29	17.91	19.09	14.92	29.81	9.38	12.96	13.83
R^{2*}	0.32	-	0.05	0.45	-	0.74	0.48	0.45	0.94	0.45	0.33	0.25	0.87	0.21	0.71	0.10
CV b %	2.85	-	4.50	11.30	-	21.32	26.17	24.29	22.54	16.33	13.38	8.57	77.85	4.87	20.18	4.59

CONCLUSION

On the basis of high inter-cluster value, crossing of genotypes of cluster II and IV could be useful to get maximum hybrid vigour and desirable segregants. Also based on mean performance and genetic distance, hybridization involving BGM 116, BGM 137 and BGM 133 (cluster II) and BGM 51 (cluster IV), should result in desirable recombinants, leading to the development of useful genetic stocks.

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Figure 1: Clustering Pattern of Different Groups with Inter-Cluster and Intra-Cluster Distance Among the Bottle Gourd Genotypes